

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 10:47:40 : Search time 202.3 Seconds
(without alignments)
2886.003 Million cell updates/sec

Title: US-09-602-833a-3
Perfect score: 681
Sequence: 1 atggaattcgtgatactgcc.....ctttagccttcaacttga 681

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: N.Geneseq_1101:*
2: /SID52/gcgdata/geneseq/geneseqn/NA1980.DAT:*
3: /SID52/gcgdata/geneseq/geneseqn/NA1981.DAT:*
4: /SID52/gcgdata/geneseq/geneseqn/NA1982.DAT:*
5: /SID52/gcgdata/geneseq/geneseqn/NA1983.DAT:*
6: /SID52/gcgdata/geneseq/geneseqn/NA1984.DAT:*
7: /SID52/gcgdata/geneseq/geneseqn/NA1985.DAT:*
8: /SID52/gcgdata/geneseq/geneseqn/NA1986.DAT:*
9: /SID52/gcgdata/geneseq/geneseqn/NA1987.DAT:*
10: /SID52/gcgdata/geneseq/geneseqn/NA1988.DAT:*
11: /SID52/gcgdata/geneseq/geneseqn/NA1989.DAT:*
12: /SID52/gcgdata/geneseq/geneseqn/NA1990.DAT:*
13: /SID52/gcgdata/geneseq/geneseqn/NA1991.DAT:*
14: /SID52/gcgdata/geneseq/geneseqn/NA1992.DAT:*
15: /SID52/gcgdata/geneseq/geneseqn/NA1993.DAT:*
16: /SID52/gcgdata/geneseq/geneseqn/NA1994.DAT:*
17: /SID52/gcgdata/geneseq/geneseqn/NA1995.DAT:*
18: /SID52/gcgdata/geneseq/geneseqn/NA1996.DAT:*
19: /SID52/gcgdata/geneseq/geneseqn/NA1997.DAT:*
20: /SID52/gcgdata/geneseq/geneseqn/NA1998.DAT:*
21: /SID52/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SID52/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	681	100.0	681	22	AAF24903	Nucleotide sequence
2	681	100.0	1116	22	AAF24902	Nucleotide sequence
3	130.4	19.1	2056	22	AAH17218	Human CDNA sequence
4	78.6	11.5	936	22	AAF58252	Oligonucleotide D1
5	78.6	11.5	936	22	AAF58254	Oligonucleotide D1
6	78.6	11.5	936	22	AAF58257	Oligonucleotide D1
7	78.6	11.5	936	22	AAF58259	Oligonucleotide D2
8	78.6	11.5	936	22	AAF58262	Oligonucleotide D2
9	78.6	11.5	936	22	AAF58255	Oligonucleotide D1
10	77.4	11.4	936	22	AAF58252	Oligonucleotide D1
11	77.4	11.4	936	22	AAF58254	Oligonucleotide D1

C 12	77.4	11.4	936	22	AAF58257	Oligonucleotide D1
C 13	77.4	11.4	936	22	AAF58259	Oligonucleotide D2
C 14	77.4	11.4	936	22	AAF58262	Oligonucleotide D2
C 15	77.4	11.4	938	22	AAF58255	Oligonucleotide D1
16	57.4	8.4	1600	22	AA161075	Human polynucleoti
17	57.4	8.4	1947	20	AAK52247	Protein PRO239 CDN
18	57.4	8.4	1947	22	AAK72405	Human secreted pro
19	57.4	8.4	2384	19	AAV30919	Human secreted pro
20	57.4	8.4	2384	22	AAK98398	Human CDNA clone A
21	57.4	8.4	2412	22	AAK59289	Human polynucleoti
22	57.4	8.4	2641	21	AAK52427	HTM clone 2709055
23	56.8	8.3	6242	21	AAK99495	Human CDNA encodin
24	55.8	8.2	2410	22	AAH14179	Human CDNA sequenc
25	55.2	8.1	3159	21	AAK99494	Human DNA encoding
26	55.2	8.1	3400	21	AAK76598	Human ORF ORF2153
27	55.2	8.1	6125	22	AAK72745	Human cervical can
28	52.6	7.7	3138	21	AAK30202	Human RING finger
29	51.8	7.6	2169	21	AAK30203	Human RING finger
30	51	7.5	1986	22	AAK26548	DNA encoding human
31	51	7.5	6470	22	AAK58376	Human polynucleoti
32	50.4	7.4	2620	22	AAH14529	Human CDNA sequenc
33	50.4	7.4	2840	22	AAH24250	Human Ras-binding
34	50.4	7.4	2847	22	AAH17735	Human CDNA sequenc
35	49.8	7.3	2694	21	AAK45671	Nucleotide sequenc
36	48.6	7.1	5199	22	AAK58164	Human polynucleoti
37	47.6	7.0	2527	22	AAK15457	Human CDNA sequenc
38	46.2	6.8	3675	21	AAK21797	Human breast and o
39	43.4	6.4	861	22	AAK06813	Human CDNA clone (
40	42.8	6.3	6703	19	AAK95836	Adenylate cyclase
41	42.4	6.2	502	21	AAK00229	Human secreted pro
42	41.8	6.1	1710	22	AAK33095	Human colon cancer
43	40.6	6.0	1273	22	AAK34612	Human colon cancer
44	39.8	5.8	1470	21	AAK78035	Human cancer assoc
45	39.8	5.8	3331	22	AAK22442	Human CDNA encodin

ALIGNMENTS

RESULT 1	
ID AAF24903	standard; CDNA; 681 BP.
XX	
AC AAF24903;	
XX	
DT 20-APR-2001	(first entry)
XX	
DE	Nucleotide sequence of a human SGT4-2 polypeptide.
XX	
KW Human; SGT4; signal transduction; guanosine triphosphate binding protein;	
KW GTP binding protein; cancer; immune response; nutritional source;	
KW animal feed; ss.	
XX	
OS Homo sapiens.	
XX	
FH	
FT	
FT CDS.	1.681
FT	/*tag= a
FT	/product= "SGT4"
PN	
XX	
PD	WO200078959-A1.
XX	
PD	28-DEC-2000.
XX	
PF	22-JUN-2000; 2000WO-US17248.
XX	
XX	
PR	23-JUN-1999; 99US-0140627.
XX	
XX	(LEXI-) LEXICON GENETICS INC.
PA	
XX	
XX	Turner AC, Zambrowicz B, Nehls M, Friedrich GA, Sands AT;
PI	
XX	
XX	WPI; 2001-032329/04.
DR	

DR P-PSDB; AAB31564.
 XX New SGT4 genes and proteins, useful for diagnosing and treating
 PT disorders involving inappropriate regulation of a signal transduction
 mechanism e.g. cancer -
 PS Claim 1; Fig 3; 82pp; English.
 XX
 CC The present sequence encodes a human SGT4 polypeptide. SGT4 polypeptides
 CC are involved in signal transduction pathways regulated by guanosine
 CC triphosphate (GTP) binding proteins). SGT4 polynucleotides and
 CC polypeptides are for diagnosing and treating conditions related to a
 CC signal transduction mechanism involving SGT4 such as cancer. In
 CC addition, it can be used to detect the expression of SGT4 as markers of
 CC specific cells and tissues such as neuronal tissue, heart, liver,
 CC pancreas and adrenal gland. They are also useful for the construction of
 CC transgenic and knockout animals for studying SGT4 function in vivo and
 CC for the screening of SGT4 (ant)agonists in an animal model. Other more
 CC general uses include: as molecular weight markers on Southern gels; as
 CC chromosome markers or tags; as probes; for selecting and making
 CC oligomers for attachment to a gene chip; to raise anti-protein or
 CC anti-DNA antibodies or to elicit immune response. They are also
 CC also be used as nutritional sources or supplements such as in animal
 CC feed.
 XX
 SQ Sequence 681 BP; 212 A; 138 C; 142 G; 189 T; 0 other;

Query Match 100.0%; Score 681; DB 22; Length 681;
 Best Local Similarity 100.0%; Pred. No. 7, 5e-198;
 Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgagaattctgagctgctgcaaaaacccaatctcaatcttcagcagagaatcggtgt 60
 DB 1 atgagaattctgagctgctgcaaaaacccaatctcaatcttcagcagagaatcggtgt 60
 QY 61 ttgagaacctgaagaactcaatggtgttcaactctcgaagaagatccctccgaa 120
 DB 61 ttgagaacctgaagaactcaatggtgttcaactctcgaagaagatccctccgaa 120
 QY 121 ttgagaatttgtaaaatctagagagactgagctgttcctggaatctagaattatgag 180
 DB 121 ttgagaatttgtaaaatctagagagactgagctgttcctggaatctagaattatgag 180
 QY 121 ttggagatgttgtaaaatctagagagactgagctgttcctggaatctagaattatgag 180
 DB 121 ttggagatgttgtaaaatctagagagactgagctgttcctggaatctagaattatgag 180
 QY 181 ctgaccttgtaaatgaatctgaagaagttacattgttagatatctcgaacaaga 240
 DB 181 ctgaccttgtaaatgaatctgaagaagttacattgttagatatctcgaacaaga 240
 QY 241 ttctcagtgctccaactgtgctcgtcgagtgctgaattgcagtggttgatatacgc 300
 DB 241 ttctcagtgctccaactgtgctcgtcgagtgctgaattgcagtggttgatatacgc 300
 QY 301 agcaataactgaccgagcctgcgcgaagatalagacaggtcagagagctcagagctt 360
 DB 301 agcaataactgaccgagcctgcgcgaagatalagacaggtcagagagctcagagctt 360
 QY 301 agcaataactgaccgagcctgcgcgaagatalagacaggtcagagagctcagagctt 360
 DB 301 agcaataactgaccgagcctgcgcgaagatalagacaggtcagagagctcagagctt 360
 QY 361 ctctgtataaaaacaagttagctacctctccattccatcgaactgaaagaagctc 420
 DB 361 ctctgtataaaaacaagttagctacctctccattccatcgaactgaaagaagctc 420
 QY 421 actctgtagtgtcgaatgaggagcatttgtagagctcccaactgaccttgtagactca 480
 DB 421 actctgtagtgtcgaatgaggagcatttgtagagctcccaactgaccttgtagactca 480
 QY 481 tccacaccttaaaatttgaagccttatgagacaatcctatgtataatgccaatgtgaa 540
 DB 481 tccacaccttaaaatttgaagccttatgagacaatcctatgtataatgccaatgtgaa 540
 QY 541 gatggcaatgaataatggaagtgaacggatgcgcaacatttgaataaagaagtatg 600
 DB 541 gatggcaatgaataatggaagtgaacggatgcgcaacatttgaataaagaagtatg 600
 QY 601 aagccatatattggaagccttaagaagaagaatctgttccagctataccaccaagtgt 660

DB 601 aagccatatattggaagccttaagaagaagaatctgttccagctataccaccaagtgt 660
 QY 661 tctttagacctcaacttga 681
 DB 661 tctttagacctcaacttga 681

RESULT 2

AAF24902
 ID AAF24902 standard; cDNA; 1116 BP.

AC AAF24902;

DT 20-APR-2001 (first entry)

DE Nucleotide sequence of a human SGT4-1 polypeptide.

KW Human; SGT4; signal transduction; guanosine triphosphate binding protein;

KW GTP binding protein; cancer; immune response; nutritional source;

KW animal feed; ss.

OS Homo sapiens.

FT Key Location/Qualifiers

FT CDS 1..1116

FT /*tag= a

FT /product= "SGT4"

PN W0200078959-A1.

PD 28-DEC-2000.

PE 22-JUN-2000; 2000WO-US17248.

PR 23-JUN-1999; 99US-0140627.

PA (LEXI-) LEXICON GENETICS INC.

PI Turner AC, Zambrowicz B, Nehls M, Friedrich GA, Sands AT;

DR WPI: 2001-032329/04.

DR P-PSDB; AAB31563.

XX New SGT4 genes and proteins, useful for diagnosing and treating

PT disorders involving inappropriate regulation of a signal transduction

PT mechanism e.g. cancer -

PS Claim 1; Fig 1; 82pp; English.

XX The present sequence encodes a human SGT4 polypeptide. SGT4 polypeptides

CC are involved in signal transduction pathways regulated by guanosine

CC triphosphate (GTP) binding proteins). SGT4 polynucleotides and

CC polypeptides are for diagnosing and treating conditions related to a

CC signal transduction mechanism involving SGT4 such as cancer. In

CC addition, it can be used to detect the expression of SGT4 as markers of

CC specific cells and tissues such as neuronal tissue, heart, liver,

CC pancreas and adrenal gland. They are also useful for the construction of

CC transgenic and knockout animals for studying SGT4 function in vivo and

CC for the screening of SGT4 (ant)agonists in an animal model. Other more

CC general uses include: as molecular weight markers on Southern gels; as

CC chromosome markers or tags; as probes; for selecting and making

CC oligomers for attachment to a gene chip; to raise anti-protein or

CC anti-DNA antibodies or to elicit immune response. They are also

CC also be used as nutritional sources or supplements such as in animal

CC feed.
 XX
 SQ Sequence 1116 BP; 343 A; 224 C; 265 G; 284 T; 0 other;

Query Match 100.0%; Score 681; DB 22; Length 1116;

Best Local Similarity 100.0%; Pred. No. 9, 7e-198;
 Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 atgagaattctgattctgccccaaaacccaattctacatcttcacgagaatcgtgtt 60
      |||
Db     436 atgagaattctgattctgccccaaaacccaattctacatcttcacgagaatcgtgtt 495
QY      61 ttgaagaacctgaagaacctcaatgtgtgttcaactatctgaagagacttcctcga 120
      |||
Db     496 ttgaagaacctgaagaacctcaatgtgtgttcaactatctgaagagacttcctcga 555
QY     121 ttggagagattgtgaaaatctagaagagacttgattgttcttggaatctagaattatgtg 180
      |||
Db     556 ttggagagattgtgaaaatctagaagagacttgattgttcttggaatctagaattatgtg 615
QY     181 ctgaccttgaatgaatgaatttgaagcaagttacattttagatatactcagaacaaag 240
      |||
Db     616 ctgaccttgaatgaatgaatttgaagcaagttacattttagatatactcagaacaaag 675
QY     241 ttttccagtgctcccaatctgtctctgcggaatgcgaatttgcagtggttgatatacgc 300
      |||
Db     676 ttttccagtgctcccaatctgtctctgcggaatgcgaatttgcagtggttgatatacgc 735
QY     301 agcaataacctgacccgaccccgcaagatatagacaggttagagagcctgcagagcttc 360
      |||
Db     736 agcaataacctgacccgaccccgcaagatatagacaggttagagagcctgcagagcttc 795
QY     361 ctctgtatataaaaacaaagttgacctacttccctattccatgctgcaacctgaaagagctc 420
      |||
Db     796 ctctgtatataaaaacaaagttgacctacttccctattccatgctgcaacctgaaagagctc 855
QY     421 actctgttagctgcagtgggagaccatttggtagagctcccaactgaccttctgtactca 480
      |||
Db     856 actctgttagctgcagtgggagaccatttggtagagctcccaactgaccttctgtactca 915
QY     481 tccaccctttaaatttgaagccttatgagacaatctctatgataatggccaatgtgaa 540
      |||
Db     916 tccaccctttaaatttgaagccttatgagacaatctctatgataatggccaatgtgaa 975
QY     541 gatggcaatgaataatgaagaatgaacggatcgccaacatttgaataagaagttatg 600
      |||
Db     976 gatggcaatgaataatgaagaatgaacggatcgccaacatttgaataagaagttatg 1035
QY     601 aaagcctatatitgaagaccttaagaagaagaatctgttcccgctataccaccaagtg 660
      |||
Db    1036 aaagcctatatitgaagaccttaagaagaagaatctgttcccgctataccaccaagtg 1095
QY     661 tcttttagccttcaacttga 681
      |||
Db    1096 tcttttagccttcaacttga 1116

```

RESULT 3

AAH17218

ID AAH17218 standard; cDNA; 2056 BP.

AC AAH17218;

DT 26-JUN-2001 (first entry)

DE Human cDNA sequence SEQ ID NO:16594.

DE Human; primer: detection; diagnosis; antisense therapy; gene therapy; ss.

OS Homo sapiens.

PN EPI074617-A2.

PD 07-FEB-2001.

PF 28-JUL-2000; 2000BP-0116126.

PR 29-JUL-1999; 99JP-0248036.

PR 27-AUG-1999; 99JP-0300253.

PR 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX

PA (HELI-) HELIX RES INST.

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX

DR WPI; 2001-318749/34.

PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX

PS Claim 8; SEQ ID 16594; 2537pp + CD ROM; English.

CC The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX

SQ Sequence 2056 BP; 642 A; 394 C; 495 G; 525 T; 0 other;

Query Match 19.1%; Score 130.4; DB 22; Length 2056;
 Best Local Similarity 99.2%; Pred. No 1.5e-29;
 Matches 131; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 550 gaataatggaagtgaaagcggatcgccaacatttgaataagaagttatgaagcctat 609
 |||
 Db 1291 gaataatggaagtgaaagcggatcgccaacatttgaataagaagttatgaagcctat 1350
 QY 610 attgaagaccttaagaagaagaagaatctgttcccgctataccaccaagtgctcttagc 669
 |||
 Db 1351 attgaagaccttaagaagaagaagaatctgttcccgctataccaccaagtgctcttagc 1410
 QY 670 cttaacttga 681
 |||
 Db 1411 cttaacttga 1422

RESULT 4

AAFS8252.

ID AAFS8252 standard; DNA; 936 BP.

AC AAFS8252;

DT 24-APR-2001 (first entry)

DE Oligonucleotide D1835.

XX Electron-transfer group; ETM; mismatch; genotyping;
 KW gene expression; ss.
 XX

OS	Synthetic.
PN	WO200107665-A2.
XX	
PD	01-FEB-2001.
XX	
PF	26-JUL-2000; 2000WO-US20476.
XX	
PR	26-JUL-1999; 99US-0145695.
PA	17-MAR-2000; 2000US-0190259.
XX	
PI	(CLIN-) CLINICAL MICRO SENSORS INC.
XX	
PT	Umek RM;
DR	WPI; 2001-159728/16.
XX	
PT	Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
XX	
PS	Example 6; Page 127; 159pp; English.
CC	The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
XX	
XX	Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;

[illegible][illegible][illegible]

```

Db 175 www..... 234
Oy 181 ctgccttgaattgaattgaagcaagtacatttgtagatctcgaacaag 240
Db 235 ..... 234
Oy 241 ttcttcaggtcccaatctgtctcgtcgatgcaattgacgtgtgatacagc 300
Db 295 ..... 354
Oy 301 agcaataacctgacgcagctgcgcgaagatagacagctagagagctgcagactt 360
Db 355 ..... 414
Oy 361 ctctgtataaaacaagttagacctcttcctattccatgctgtaaccgaagaagctc 420
Db 415 ..... 474
Oy 421 actctgtagctgcagtgaggacatttggtagctcccaactgaccttgtagctca 480
Db 475 ..... 534
Oy 481 tccacaccttaaatctgtaagcctatggaacatcctattgataatgcccaatgtgaa 540
Db 535 ..... 594
Oy 541 gatggcaatgaataatggaagtgaacggatcgcaacatttgataagaagtattg 600
Db 595 ..... 654
Oy 601 aaagcctatattgaagaccttaagaagaagaatctgtccacgatacaccaagt 660
Db 655 ..... 714
Oy 661 tctttaagccttcaactt 679
Db 715 ..... 733

RESULT 6
AAF58257
ID AAF58257 standard; DNA; 936 BP.
XX
AC AAF58257;
XX
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide D1954.
XX
KW Electron-transfer group; ETW; mismatch; genotyping;
XX
OS Synthetic.
XX
PN WO200107665-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000HO-US20476.
XX
PR 26-JUL-1999; 990S-0145695.
XX
PR 17-MAR-2000; 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI umek RM;
XX
DR WPI; 2001-159728/16.
XX
PT Nucleic acids containing electron-transfer group, useful as labels in
XX hybridization assays, e.g. for genotyping, allowing repeat analyses on
XX a single surface
XX

```

```

PS Example 6; Page 127; 159pp; English.
XX
CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETW) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
SQ Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;

Query Match 11.5%; Score 78.6; DB 22; Length 936;
Best Local Similarity 0.9%; Pred. No. 6.3e-14;
Matches 6; Conservative 397; Mismatches 276; Indels 0; Gaps 0;

Oy 1 atgagaattcgtatcgtccaaaaaacaaatctcacatcttcacagagaatcggtgt 60
Db 55 ..... 114
Oy 61 ttgaagacctgaagaacctcaatgtggttcaactatctgaagagcattcctccgaa 120
Db 115 ..... 174
Oy 121 ttggagatttgaanaatcagagagctgattgttctggaatctagaattaatgag 180
Db 175 ..... 234
Oy 181 ctgccttgaatgaatgaatgaagcaagttacattgtatgatalccgaacaag 240
Db 235 ..... 294
Oy 241 ttcttcaggtcccaatctgtctcgtcgatgctgaatttgcaagtggttgatcagc 300
Db 295 ..... 354
Oy 301 agcaataacctgacgcagctgcgcgaagatagacagctagagagctgcagactt 360
Db 355 ..... 414
Oy 361 ctctgtataaaacaagttagacctcttcctattccatgctgaacctgaagaagctc 420
Db 415 ..... 474
Oy 421 actctgttagctgcaagtgggacatttggtagagctcccaactgaccttgtagctca 480
Db 475 ..... 534
Oy 481 tccacaccttaaatctgtaagcctatggaacatcctattgataatgcccaatgtgaa 540
Db 535 ..... 594
Oy 541 gatggcaatgaataatggaagtgaacggatcgcaacatttgataagaagtattg 600
Db 595 ..... 654
Oy 601 aaagcctatattgaagaccttaagaagaagaatctgtccacgatacaccaagt 660
Db 655 ..... 714
Oy 661 tctttaagccttcaactt 679
Db 715 ..... 733

RESULT 7
AAF58259
ID AAF58259 standard; DNA; 936 BP.
XX
AC AAF58259;
XX
DT 24-APR-2001 (first entry)
XX

```

```

DE      Oligonucleotide D2004.
XX
XX      Electron-transfer group: ETM; mismatch; genotyping:
KM      gene expression; ss.
XX
XX      Synthetic.
XX      WO200107665-A2.
XX      PD
XX      01-FEB-2001.
XX
XX      26-JUL-2000; 2000WO-US20476.
XX      PF
XX      26-JUL-1999; 99US-0145695.
XX      PR
XX      17-MAR-2000; 2000US-0190259.
XX
XX      (CLIN-) CLINICAL MICRO SENSORS INC.
XX
XX      Umek RM;
XX
XX      WPI: 2001-159728/16.
XX
XX      Nucleic acids containing electron-transfer group, useful as labels in
XX      hybridization assays, e.g. for genotyping, allowing repeat analyses on
XX      a single surface.
XX
XX      Example 6: Page 128; 159pp; English.
XX
XX      The present invention relates to a composition comprising two nucleic
XX      acids each containing an electron-transfer group (ETM) having
XX      different redox potentials. The invention is used for electronic
XX      detection of nucleic acids, especially of substitutions (mismatches)
XX      and single-nucleotide polymorphisms, e.g. for genotyping,
XX      monitoring gene expression.
XX
XX      Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;
SQ

```

OY	401	tcacacaccttaaaattgttaagcctcatgagacaatccttatgataatgcccattgtgaa	540	
Db	535	#####	594	
OY	541	gatgcaatgaataatbgaagtgaacgagatcgccaacatttgaataagaattatg	600	
Db	555	#####	654	
OY	601	aagcctataattgaagaccttaagaaagaaatcgttcccgagctataccaccaagt	660	
Db	655	#####	714	
OY	661	tctttagcctcaacttt	679	
Db	715	#####	733	
RESULT 8				
AF58262				
ID	AAF58262 standard; DNA; 936 BP.			
AC	AAF58262;			
XX				
DT	24-APR-2001 (first entry)			
XX				
DE	Oligonucleotide D2007.			
XX				
KW	Electron-transfer group; ETM; mismatch; genotyping;			
KW	gene expression; ss.			
XX				
OS	Synthetic.			
XX				
PN	WO200107665-A2.			
XX				
PD	01-FEB-2001.			
PF	26-JUL-2000; 2000WO-US20476.			
XX				
PR	26-JUL-1999; 99US-0145695.			
XX	17-MAR-2000; 2000US-0190299.			
PA	(CLIN-) CLINICAL MICRO SENSORS INC.			
XX				
PI	Umek RM;			
DR	WPI: 2001-159728/16.			
XX				
PT	Nucleic acids containing electron-transfer group, useful as labels in			
PT	hybridization assays, e.g. for genotyping, allowing repeat analyses o			
XX	a single surface -			
XX				
PS	Example 6; Page 128; 159pp; English.			
XX				
CC	The present invention relates to a composition comprising two nucleic			
CC	acids each containing an electron-transfer group (ETM) having			
CC	different redox potentials. The invention is used for electronic			
CC	detection of nucleic acids, especially of substitutions (mismatches)			
CC	and single-nucleotide polymorphisms, e.g. for genotyping,			
CC	monitoring gene expression.			
XX				
SQ	Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;			
Query Match 11.5%; Score 78.6; DB 22; Length 936;				
Best Local Similarity 0.9%, Pred. NO. 6.3e-14;				
Matches 6; Conservative 397; Mismatches 276; Indels 0; Gaps				
OY	1 atgaagaattcggatcgcgcaaaaacccaatctcacatcttccagcagaagaatcggtgt			60
Db	#####			114
OY	61 ttgaagaacctgaagaactcaatgtyggttcaactatgaagacattcctccagaa			120

XX	AAF58252;
AC	
XX	
DT	24-APR-2001 (first entry)
XX	
DE	Oligonucleotide D1835.
XX	
KW	Electron-transfer group; ETW; mismatch; genotyping;
KW	gene expression; ss.
XX	
OS	Synthetic.
XX	
PN	W0200107665-A2.
XX	
PD	01-FEB-2001.
XX	
PF	26-JUL-2000; 2000WO-US20476.
XX	
PR	26-JUL-1999; 99US-0145695.
PR	17-MAR-2000; 2000US-0190259.
XX	
PA	(CLIN-) CLINICAL MICRO SENSORS INC.
XX	
PI	Unek RM;
DR	WPI; 2001-159728/16.
XX	
PT	Nucleic acids containing electron-transfer group, useful as labels in
PT	hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT	a single surface -
XX	
PS	Example 6; Page 127; 159pp; English.
XX	
CC	The present invention relates to a composition comprising two nucleic
CC	acids each containing an electron-transfer group (ETW) having
CC	different redox potentials. The invention is used for electronic
CC	detection of nucleic acids, especially of substitutions (mismatches)
CC	and single-nucleotide polymorphisms, e.g. for genotyping,
CC	monitoring gene expression.
XX	
XX	Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;

Query Match 11.4%, Score 77.4; DB 22; Length 936;
Best Local Similarity 0.9%, Pred. No. 1,5e-13;
Matches 6; Conservative 390; Mismatches 17; Indels 0; Gaps 0.

Db	415	www.....TAAAGC.....	356
Qy	421	aactcgttagctgcgaaggagaccatttggtagagctcccaactgaccttggactca	480
Db	335	www.....	296
Qy	481	tcacaaccttaaaattgttaagccctatgagacaatccatlgataatgcgaatgtgaa	540
Db	295	www.....	236
Qy	541	gatggcaatggaataatggaagtgaacggatcgccaacatttgaataagaagtatg	600
Db	235	www.....	176
Qy	601	aaagcctataatgagaaccttaagaagaagaaatcgtlcccaactatacaccacaagt	660
Db	175	www.....	116
Qy	661	tccttta 667	
Db	115	www.....	109

XX	RESULT	11
XX	AAF58254/C	
ID	AAF58254 standard; DNA: 936 BP.	
XX		
AC	AAF58254;	
XX		
DT	24-APR-2001 (first entry)	
XX		
DE	O11gonucleotide D1875.	
XX		
KW	Electron-transfer group; ETM; mismatch; genotyping;	
KW	gene expression, ss.	
XX		
OS	Synthetic.	
XX		
PN	WO200107665-A2.	
XX		
PD	01-FEB-2001.	
XX		
PE	26-JUL-2000; 2000WO-US20476.	
XX		
PR	26-JUL-1999; 99US-0145695.	
PR	17-MAR-2000; 2000US-0190259.	
XX		
PA	(CLIN-) CLINICAL MICRO SENSORS INC.	
XX		
P1	Umek RM;	
XX		
DR	WPI; 2001-159728/16.	
XX		
XX		
PT	Nucleic acids containing electron-transfer group, useful as labels in	
PT	hybridization assays, e.g. for genotyping, allowing repeat analyses on	
PT	a single surface	
XX		
PS		
XX	Example 6; Page 127; 159pp; English.	
XX		
CC	The present invention relates to a composition comprising two nucleic	
CC	acids each containing an electron-transfer group (ETM) having	
CC	different redox potentials. The invention is used for electronic	
CC	detection of nucleic acids, especially of substitutions (mismatches)	
CC	and single-nucleotide polymorphisms, e.g. for genotyping,	
CC	monitoring gene expression.	
XX		
XX		
SO	Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;	
	Query Match	11.4%; Score 77.4; DB 22; Length 936;
	Best Local Similarity	0.9%; Pred. No. 1.5e-13;
Matches	6; Conservative 390; Mismatches 271; Indels 0; Gaps 0;	


```
RESULT 13
AAF58259/c
ID AAF58259 standard; DNA; 936 BP.
XX
AC AAF58259;
XX
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide D2004.
XX
KW Electron-transfer group; ETM; mismatch; genotyping;
KM gene expression; ss.
XX
OS Synthetic.
XX
PN WO200107665-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-US20476.
XX
PR 26-JUL-1999; 99US-0145695.
XX
PR 17-MAR-2000; 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI Umek RM;
XX
DR WPI: 2001-159728/16.
XX
PT Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface
XX
XX
PS Example 6; Page 128; 159pp; English.
XX
CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
SQ Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;

Query Match 11.4%; Score 77.4; DB 22; Length 936;
Best Local Similarity 0.9%; Pred. No. 1.5e-13;
Matches 6; Conservative 390; Mismatches 271; Indels 0; Gaps 0;

QY 1 atgaaatctggaatctgcaaaacaaatctcacatctccagagaaatcggtgt 60
DB 775 www.....
QY 61 ttgaagaacctgaagaacctcaatggtttcaactctgaagagcatctccagaa 120
DB 715 www.....
QY 121 ttggagagctgtgaaacctgagagactgattgtctctggaacctgaatattgag 180
DB 655 www.....
QY 181 ctgccttgaattgaattgaagaagtaacattgtagatctgacagaacaaag 240
DB 595 www.....
QY 241 ttcttcagttcccaatctgtctctgcgagatgtcgaatttcagtggttgatatacgc 300
DB 535 www.....
QY 301 agcataaaccctgaccgacctccgcagaatatagacaggtcagagagctt 360
```

```
DB 475 .....
QY 361 cctctgtataaaacaaagttagacctctccatctccatgctgaacctgaagaagctc 420
DB 415 .....
QY 421 actctgtagctgcagtgagacacattggtgagctcccaactgacctgtgactca 480
DB 355 .....
QY 481 tccacaccttataaattgtgaagccttalgacaaatcctattgataaagcccaatgtga 540
DB 295 www.....
QY 541 gatcgcaatgaataatgaagaatgaaagcgagatcgcaacatttgaataaagattag 600
DB 235 www.....
QY 601 aaagcctalatggaagacctaaagaagaagaaatctgttccagctataccaccaagtg 660
DB 175 .....
QY 661 tcttlla 667
DB 115 www.....

RESULT 14
AAF58262/c
ID AAF58262 standard; DNA; 936 BP.
XX
AC AAF58262;
XX
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide D2007.
XX
KW Electron-transfer group; ETM; mismatch; genotyping;
KM gene expression; ss.
XX
OS Synthetic.
XX
PN WO200107665-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-US20476.
XX
PR 26-JUL-1999; 99US-0145695.
XX
PR 17-MAR-2000; 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI Umek RM;
XX
DR WPI: 2001-159728/16.
XX
PT Nucleic acids containing electron-transfer group (ETM) having
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface
XX
XX
PS Example 6; Page 128; 159pp; English.
XX
CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
SQ Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;
```


Db 175 WWWWWW 116
QY 661 tcttla 667
: : : : :
Db 115 WWWWWW 109

Search completed: February 26, 2002, 10:47:46
Job time: 10583 sec